#2

OIPE

RAW SEQUENCE LISTING   DATE: 01/28/2002
PATENT APPLICATION: US/10/006,394   TIME: 11:32:53

Input Set : N:\Crf3\RULE60\10006394.raw
Output Set: N:\CRF3\01282002\J006394.raw

SEQUENCE LISTING

```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Yi Li and Mark D. Adams
 7     (ii) TITLE OF INVENTION: Human G-Protein Receptor HIBEF51
 9    (iii) NUMBER OF SEQUENCES: 10
11     (iv) CORRESPONDENCE ADDRESS:
13          (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
14                         Cecchi, Stewart & Olstein
15          (B) STREET: 6 Becker Farm Road
16          (C) CITY: Roseland
17          (D) STATE: NJ
18          (E) COUNTRY: US
19          (F) ZIP: 07068-1739
21      (v) COMPUTER READABLE FORM:
22          (A) MEDIUM TYPE: Floppy disk
23          (B) COMPUTER: IBM PC compatible
24          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25          (D) SOFTWARE: WordPerfect 5.1
27     (vi) CURRENT APPLICATION DATA:
28          (A) APPLICATION NUMBER: US/10/006,394
29          (B) FILING DATE: 10-Dec-2001
30          (C) CLASSIFICATION:
32    (vii) PRIOR APPLICATION DATA:
33          (A) APPLICATION NUMBER: 09/228,420
34          (B) FILING DATE:
36   (viii) ATTORNEY/AGENT INFORMATION:
37          (A) NAME: MULLINS, J.G.
38          (B) REGISTRATION NUMBER: 33073
39          (C) REFERENCE/DOCKET NUMBER: 325800-453 (PF187)
41     (ix) TELECOMMUNICATION INFORMATION:
42          (A) TELEPHONE: 201-994-1700
43          (B) TELEFAX: 201-994-1744
46 (2) INFORMATION FOR SEQ ID NO: 1:
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 2764 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: single
52          (D) TOPOLOGY: linear
54     (ii) MOLECULE TYPE: cDNA
57     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
59 AATTACAGGT AACATTCTGA AATTGAACTA AACAGTAAAT TCTGTTGAAA TGTTTTCAAA     60
61 GAGGCAAAAT ATTATATTGG AATCAATGAA GAAAGTAAAT TATCTTGGCT AATTTTATTA    120
63 GTGGTAATTG TAGTGAAAGG TTTTCCTAAA TATTATAAGC AAATTCCTTT TCTCCCCCGT    180
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C--> 28
C--> 29

ENTERED

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 65 CTCAAATGAA AGGAAATGGG GGTAAATTAA TCTGACTGTG ATTGGTTTTG TTTTATGCTG   240
 67 ATCTTGAAAG CTTGATGTTG CTGCTGCTCC TCATACAGTA CAGATCAGTT GTGTGGGGTG   300
 69 CTATTGAGGG TAGCCGTGAA TAGTGGTGCC AGTAGGGGTG GAGCGGGAGG GATGATGCCA   360
 71 GCCTGAGCTA GCCAGGTTCT TTGATTAGGG CATTGGATGT GAAATGTAAA ATGCTCTCTC   420
 73 CTTTTCTTCT ATCAGCTGTT CAGAGGAGAC TCATTACAAC TCCTGCTGAA GCTCCTAATC   480
 75 TTCTTCCCTT CTCTTCTACC CTTTCCCCCT ACCCTCACTT GGCCTGAAGA CGTTCTCCCC   540
 77 AGAGTTTACC TTGCTCCCCT GGTGCTATGT GTATGGTGAA CCTGGCACTA TGGCCGCGTC   600
 79 TGGGACTGGC CAGACAACTG CTGCTGGCTC TCCTTATTCC AGGAAGGATT TAAAGGGGAA   660
 81 TTGCACTGCA GGCAATGCAC CAGAGCAGCA GCATCAGGAG CTTGGGGAGT AAGGCTCCTC   720
 83 TGGCATTATT ACACACATGC AAAGCTGACC GCAATGACAG CAGCTGCTTC TTTGAACTGT   780
 85 TGGCAGCAGC CAAGCGGCAG CATGAAGTGA CAGATCACTC CTGAGCTCAA G ATG AAC   837
 86                                                         Met Asn
 88 TCC ACC TTG GAT GGT AAT CAG AGC AGC CAC CCT TTT TGC CTC TTG GCA   885
 89 Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu Leu Ala
 90          5                   10                  15
 92 TTT GGC TAT TTG GAA ACT GTC AAT TTT TGC CTT TTG GAA GTA TTG ATT   933
 93 Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu Val Leu Ile
 94         20                  25                  30
 96 ATT GTC TTT CTA ACT GTA TTG ATT ATT TCT GGC AAC ATC ATT GTG ATT   981
 97 Ile Val Phe Leu Thr Val Leu Ile Ile Ser Gly Asn Ile Ile Val Ile
 98 35                  40                  45                  50
100 TTT GTA TTT CAC TGT GCA CCT TTG TTG AAC CAT CAC ACT ACA AGT TAT  1029
101 Phe Val Phe His Cys Ala Pro Leu Leu Asn His His Thr Thr Ser Tyr
102                 55                  60                  65
104 TTT ATC CAG ACT ATG GCA TAT GCT GAC CTT TTT GTT GGG GTG AGC TGC  1077
105 Phe Ile Gln Thr Met Ala Tyr Ala Asp Leu Phe Val Gly Val Ser Cys
106                 70                  75                  80
108 GTG GTC CCT TCT TTA TCA CTC CTC CAT CAC CCC CTT CCA GTA GAG GAG  1125
109 Val Val Pro Ser Leu Ser Leu Leu His His Pro Leu Pro Val Glu Glu
110         85                  90                  95
112 TCC TTG ACT TGC CAG ATA TTT GGT TTT GTA GTA TCA GTT CTG AAG AGC  1173
113 Ser Leu Thr Cys Gln Ile Phe Gly Phe Val Val Ser Val Leu Lys Ser
114 100                 105                 110
116 GTC TCC ATG GCT TCT CTG GCC TGT ATC AGC ATT GAT AGA TAC ATT GCC  1221
117 Val Ser Met Ala Ser Leu Ala Cys Ile Ser Ile Asp Arg Tyr Ile Ala
118 115                 120                 125                 130
120 ATT ACT AAA CCT TTA ACC TAT AAT ACT CTG GTT ACA CCC TGG AGA CTA  1269
121 Ile Thr Lys Pro Leu Thr Tyr Asn Thr Leu Val Thr Pro Trp Arg Leu
122                 135                 140                 145
124 CGC CTG TGT ATT TTC CTG ATT TGG CTA TAC TCG ACC CTG GTC TTC CTG  1317
125 Arg Leu Cys Ile Phe Leu Ile Trp Leu Tyr Ser Thr Leu Val Phe Leu
126                 150                 155                 160
128 CCT TCC TTT TTC CAC TGG GGC AAA CCT GGA TAT CAT GGA GAT GTG TTT  1365
129 Pro Ser Phe Phe His Trp Gly Lys Pro Gly Tyr His Gly Asp Val Phe
130             165                 170                 175
132 CAG TGG TGT GCG GAG TCC TGG CAC ACC GAC TCC TAC TTC ACC CTG TTC  1413
133 Gln Trp Cys Ala Glu Ser Trp His Thr Asp Ser Tyr Phe Thr Leu Phe
134 180                 185                 190
136 ATC GTG ATG ATG TTA TAT GCC CCA GCA GCC CTT ATT GTC TGC TTC ACC  1461
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137 Ile Val Met Met Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys Phe Thr
138 195                     200             205             210
140 TAT TTC AAC ATC TTC CGC ATC TGC CAA CAG CAC ACA AAG GAT ATC AGC     1509
141 Tyr Phe Asn Ile Phe Arg Ile Cys Gln Gln His Thr Lys Asp Ile Ser
142                 215             220                 225
144 GAA AGG CAA GCC CGC TTC AGC AGC CAG AGT GGG GAG ACT GGG GAA GTG     1557
145 Glu Arg Gln Ala Arg Phe Ser Ser Gln Ser Gly Glu Thr Gly Glu Val
146             230             235                 240
148 CAG GCC TGT CCT GAT AAG CGC TAT GCC ATG GTC CTG TTT CGA ATC ACT     1605
149 Gln Ala Cys Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg Ile Thr
150         245             250                 255
152 AGT GTA TTT TAC ATC CTC TGG TTG CCA TAT ATC ATC TAC TTC TTG TTG     1653
153 Ser Val Phe Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe Leu Leu
154     260             265             270
156 GAA AGC TCC ACT GGC CAC AGC AAC CGC TTC GCA TCC TTC TTG ACC ACC     1701
157 Glu Ser Ser Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu Thr Thr
158 275             280             285                 290
160 TGG CTT GCT ATT AGT AAC AGT TTC TGC AAC TGT GTA ATT TAT AGT CTC     1749
161 Trp Leu Ala Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr Ser Leu
162             295             300                 305
164 TCC AAC AGT GTA TTC CAA AGA GGA CTA AAG CGC CTC TCA GGG GCT ATG     1797
165 Ser Asn Ser Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly Ala Met
166             310             315                 320
168 TGT ACT TCT TGT GCA AGT CAG ACT ACA GCC AAC GAC CCT TAC ACA GTT     1845
169 Cys Thr Ser Cys Ala Ser Gln Thr Thr Ala Asn Asp Pro Tyr Thr Val
170             325             330                 335
172 AGA AGC AAA GGC CCT CTT AAT GGA TGT CAT ATC TGAAGTGGCT CAGTTACGGG     1898
173 Arg Ser Lys Gly Pro Leu Asn Gly Cys His Ile
174     340                 345
176 GTTCCCGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT ATTTTATCTC TAAGTATTCC     1958
178 TAATTCACTA GGAAATCTGG GACAGAATAC TTTGACTCTA AACAATAGCA TACAAATTAT      2018
180 TCGTATGGAT ACCTTCTAAG TTTGTAGAAA TGGTTTTCCC AAGTGCTTGT GAATTAGAAG     2078
182 ACTCAAGATC ATGAAGACAA ATTGCTCTTG CTCTCAATTT TTGAAATGTC TTGGAAATGA     2138
184 CTACAGTTCT CAGATTTAAA ATGAATAAAG CCATATCTAA CACCTCTTTC CAGCTGGCAT     2198
186 GACTGAACCT GAGTGTGAAA AGCGTCAGCA TTTTAAAAAG TCATCACTTT CTTGTCACTT     2258
188 TCTGGGCTCT TTCCAGCTAT TTGGGCGTCA TATGCAATTG ATTTCTTCTA ACGGAATAGT     2318
190 AAAATATAAA TGAAAAGGTT TTAGAAATTA CTTTTTATGT ATGCCAAAGC ATAACTACAC     2378
192 TGCAAGTTTC AACACTGTCA TTTAGAAAGC CAAATGTTCT GTGTTTTATT CTCTTGAGAG     2438
194 AATTCTCAGT AGGGTGAATA ATGTGAACAC ATAAACATTA ATTTTAGAAT TTTACAGTGA     2498
196 ACCATGAAGC AAAAGTGCAA TCAAATTATA CAATTTATGA AAAACTGAGC TACTTTTTGT     2558
198 GCCATGCTTC ACAGAGATCT AAAGATATGT GTGCGTAGAA GTAATCGTGT AGTACTTTTG     2618
200 CCCATGCCTT TGTGTTATGT CTATATTTAG AATATCTGAA TTGTTAGATT TCTCTTTTAC     2678
202 AGCAAAATGT GCTTAAGCTA AAAAGTAATT CAGGGAATTC GATATCAAGC TTATCGATAC     2738
204 CGTCGACCTC GAGGGGGGGC CCGGTA                                         2764
208 (2) INFORMATION FOR SEQ ID NO: 2:
210     (i) SEQUENCE CHARACTERISTICS:
211         (A) LENGTH: 349 amino acids
212         (B) TYPE: amino acid
213         (D) TOPOLOGY: Linear
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215   (ii) MOLECULE TYPE: protein
217   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
219 Met Asn Ser Thr Leu Asp Gly Asn Gln Ser Ser His Pro Phe Cys Leu
220   5   10   15
221 Leu Ala Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu Val
222   20   25   30
223 Leu Ile Ile Val Phe Leu Thr Val Leu Ile Ile Ser Gly Asn Ile Ile
224   35   40   45
225 Val Ile Phe Val Phe His Cys Ala Pro Leu Leu Asn His His Thr Thr
226   50   55   60
227 Ser Tyr Phe Ile Gln Thr Met Ala Tyr Ala Asp Leu Phe Val Gly Val
228 65   70   75   80
229 Ser Cys Val Val Pro Ser Leu Ser Leu Leu His His Pro Leu Pro Val
230   85   90   95
231 Glu Glu Ser Leu Thr Cys Gln Ile Phe Gly Phe Val Val Ser Val Leu
232   100   105   110
233 Lys Ser Val Ser Met Ala Ser Leu Ala Cys Ile Ser Ile Asp Arg Tyr
234   115   120   125
235 Ile Ala Ile Thr Lys Pro Leu Thr Tyr Asn Thr Leu Val Thr Pro Trp
236   130   135   140
237 Arg Leu Arg Leu Cys Ile Phe Leu Ile Trp Leu Tyr Ser Thr Leu Val
238 145   150   155   160
239 Phe Leu Pro Ser Phe Phe His Trp Gly Lys Pro Gly Tyr His Gly Asp
240   165   170   175
241 Val Phe Gln Trp Cys Ala Glu Ser Trp His Thr Asp Ser Tyr Phe Thr
242   180   185   190
243 Leu Phe Ile Val Met Met Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys
244   195   200   205
245 Phe Thr Tyr Phe Asn Ile Phe Arg Ile Cys Gln Gln His Thr Lys Asp
246   210   215   220
247 Ile Ser Glu Arg Gln Ala Arg Phe Ser Ser Gln Ser Gly Glu Thr Gly
248 225   230   235   240
249 Glu Val Gln Ala Cys Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg
250   245   250   255
251 Ile Thr Ser Val Phe Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe
252   260   265   270
253 Leu Leu Glu Ser Ser Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu
254   275   280   285
255 Thr Thr Trp Leu Ala Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr
256   290   295   300
257 Ser Leu Ser Asn Ser Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly
258 305   310   315   320
259 Ala Met Cys Thr Ser Cys Ala Ser Gln Thr Thr Ala Asn Asp Pro Tyr
260   325   330   335
261 Thr Val Arg Ser Lys Gly Pro Leu Asn Gly Cys His Ile
262   340   345
266 (2) INFORMATION FOR SEQ ID NO: 3:
268   (i) SEQUENCE CHARACTERISTICS:
269   (A) LENGTH: 358 amino acids

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        270             (B) TYPE: amino acid
        271             (C) STRANDEDNESS: Not Relevant
W--> 272             (D) TOPOLOGY: Not Relevant
        274      (ii) MOLECULE TYPE: protein
        276      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
W--> 278 Met Asn Ser Thr Leu Xaa Asp Gly Asn Gln Ser Ser His Pro Phe Cys
        279                  5                 10                 15
        280 Leu Leu Ala Phe Gly Tyr Leu Glu Thr Val Asn Phe Cys Leu Leu Glu
        281                 20                 25                 30
W--> 282 Val Leu Ile Ile Val Xaa Xaa Xaa Xaa Phe Leu Thr Val Leu Ile Ile
        283                 35                 40                 45
        284 Ser Gly Asn Ile Ile Val Ile Phe Val Phe His Cys Ala Pro Leu Leu
        285         50                 55                 60
        286 Asn His His Thr Thr Ser Tyr Phe Ile Gln Thr Met Ala Tyr Ala Asp
        287 65                 70                 75                 80
        288 Leu Phe Val Gly Val Ser Cys Val Val Pro Ser Leu Ser Leu Leu His
        289             85                 90                 95
W--> 290 His Pro Leu Pro Xaa Xaa Val Glu Glu Ser Leu Thr Cys Gln Ile Phe
        291         100                 105                 110
        292 Gly Phe Val Val Ser Val Leu Lys Ser Val Ser Met Ala Ser Leu Ala
        293         115                 120                 125
        294 Cys Ile Ser Ile Asp Arg Tyr Ile Ala Ile Thr Lys Pro Leu Thr Tyr
        295         130                 135                 140
        296 Asn Thr Leu Val Thr Pro Trp Arg Leu Arg Leu Cys Ile Phe Leu Ile
        297 145                 150                 155                 160
        298 Trp Leu Tyr Ser Thr Leu Val Phe Leu Pro Ser Phe Phe His Trp Gly
        299             165                 170                 175
        300 Lys Pro Gly Tyr His Gly Asp Val Phe Gln Trp Cys Ala Glu Ser Trp
        301             180                 185                 190
W--> 302 Xaa Xaa Xaa His Thr Asp Ser Tyr Phe Thr Leu Phe Ile Val Met Met
        303         195                 200                 205
        304 Leu Tyr Ala Pro Ala Ala Leu Ile Val Cys Phe Thr Tyr Phe Asn Ile
        305         210                 215                 220
W--> 306 Phe Arg Ile Cys Gln Gln His Thr Lys Asp Ile Ser Glu Arg Xaa Xaa
        307 225                 230                 235                 240
W--> 308 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Ala Arg Phe Ser
        309             245                 250                 255
W--> 310 Ser Gln Ser Gly Xaa Xaa Xaa Xaa Glu Thr Gly Glu Val Gln Ala Cys
        311             260                 265                 270
        312 Pro Asp Lys Arg Tyr Ala Met Val Leu Phe Arg Ile Thr Ser Val Phe
        313         275                 280                 285
        314 Tyr Ile Leu Trp Leu Pro Tyr Ile Ile Tyr Phe Leu Leu Glu Ser Ser
        315         290                 295                 300
        316 Thr Gly His Ser Asn Arg Phe Ala Ser Phe Leu Thr Thr Trp Leu Ala
        317 305                 310                 315                 320
        318 Ile Ser Asn Ser Phe Cys Asn Cys Val Ile Tyr Ser Leu Ser Asn Ser
        319             325                 330                 335
        320 Val Phe Gln Arg Gly Leu Lys Arg Leu Ser Gly Ala Met Cys Thr Ser
        321             340                 345                 350
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VERIFICATION SUMMARY   DATE: 01/28/2002
PATENT APPLICATION: US/10/006,394   TIME: 11:32:54

Input Set : N:\Crf3\RULE60\10006394.raw
Output Set: N:\CRF3\01282002\J006394.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:272 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:333 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4